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<110> Ebner et al.

<120> Human Ependymin

<130> PF403D2

<150> US 10/187,904

<151> 2002-07-03

<150> US 09/229,583

<151> 1999-01-13

<150> US 60/071,330

<151> 1998-01-14

<150> US 60/075,278

<151> 1998-02-19

<160> 20

<170> PatentIn version 3.1

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tcgcgcgtcc ggatctcaaa agcggcagag gccaccgaag ggacaggaag cactttggtc 180
cagaccacac tccccgcaca gtgcggaaag agccggcggg agccactctg atccccggacg 240
cctcagcgcc cccttgggct tgggcttgcc ctcgggccgg ggaaggctga ccgcg atg 298
                                     Met
cca gga cgc gct ccc ctc cgc acc gtc ccg ggc gcc ctg ggt gcc tgg 346
Pro Gly Arg Ala Pro Leu Arg Thr Val Pro Gly Ala Leu Gly Ala Trp
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ctg ctg ggc ggc ctc tgg gcc tgg acc ctg tgc ggc ctg tgc agc ctg	394
Leu Leu Gly Gly Leu Trp Ala Trp Thr Leu Cys Gly Leu Cys Ser Leu	
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Gly Ala Val Gly Ala Pro Arg Pro Cys Gln Ala Pro Gln Gln Trp Glu	
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ggg cgc cag gtt atg tac cag caa agt agc ggg cgc aac agc cgc gcc	490
Gly Arg Gln Val Met Tyr Gln Gln Ser Ser Gly Arg Asn Ser Arg Ala	
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ctg ctc tcc tac gac ggg ctc aac cag cgc gtg cgg gtg ctg gac gag	538
Leu Leu Ser Tyr Asp Gly Leu Asn Gln Arg Val Arg Val Leu Asp Glu	
30 35 40	
agg aag gcg ctg atc ccc tgc aag aga tta ttt gaa tat att ttg ctg	586
Arg Lys Ala Leu Ile Pro Cys Lys Arg Leu Phe Glu Tyr Ile Leu Leu	
45 50 55 60	
tat aag gat gga gtg atg ttt cag att gac caa gcc acc aag cag tgc	634
Tyr Lys Asp Gly Val Met Phe Gln Ile Asp Gln Ala Thr Lys Gln Cys	
65 70 75	
tca aag atg acc ctg aca cag ccc tgg gat cct ctt gac att cct caa	682
Ser Lys Met Thr Leu Thr Gln Pro Trp Asp Pro Leu Asp Ile Pro Gln	
80 85 90	
aac tcc acc ttt gaa gac cag tac tcc att ggg ggg cct cag gag cag	730
Asn Ser Thr Phe Glu Asp Gln Tyr Ser Ile Gly Gly Pro Gln Glu Gln	
95 100 105	
atc acc gtc cag gag tgg tcg gac aga aag tca gct aga tcc tat gaa	778
Ile Thr Val Gln Glu Trp Ser Asp Arg Lys Ser Ala Arg Ser Tyr Glu	
110 115 120	
acc tgg att ggc atc tat aca gtc aag gat tgc tat cct gtc cag gaa	826
Thr Trp Ile Gly Ile Tyr Thr Val Lys Asp Cys Tyr Pro Val Gln Glu	
125 130 135 140	
acc ttt acc ata aac tac agt gtg ata ttg tct acg cgg ttt ttt gac	874
Thr Phe Thr Ile Asn Tyr Ser Val Ile Leu Ser Thr Arg Phe Phe Asp	
145 150 155	
atc cag ctg ggt att aaa gac ccc tcg gtg ttt acc cct cca agc acg	922
Ile Gln Leu Gly Ile Lys Asp Pro Ser Val Phe Thr Pro Pro Ser Thr	
160 165 170	
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Cys Gln Met Ala Gln Leu Glu Lys Met Ser Glu Asp Cys Ser Trp	
175 180 185	
tgagcctgtg cataggggaag cggcagcatc ggatgtcagc cccctgcggc cccagctgga	1027
gatggatatg agactagtca agatgtgaat gctaattgga gagaaatata attttaggaa	1087
gatgcacatt gatgtggggt tttgatgtgt ctgattttga ctactcaagc tctgtttaca	1147
gaagaaaatt gaatggcgag ggtgtggcca tatgaactga ctagatggct aatatggaca	1207

Glu	Gly	Arg	Gln	Val	Met	Tyr	Gln	Gln	Ser	Ser	Gly	Arg	Asn	Ser	Arg
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Ala	Leu	Leu	Ser	Tyr	Asp	Gly	Leu	Asn	Gln	Arg	Val	Arg	Val	Leu	Asp
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Glu	Arg	Lys	Ala	Leu	Ile	Pro	Cys	Lys	Arg	Leu	Phe	Glu	Tyr	Ile	Leu
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Leu	Tyr	Lys	Asp	Gly	Val	Met	Phe	Gln	Ile	Asp	Gln	Ala	Thr	Lys	Gln
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Cys	Ser	Lys	Met	Thr	Leu	Thr	Gln	Pro	Trp	Asp	Pro	Leu	Asp	Ile	Pro
				80					85					90	
Gln	Asn	Ser	Thr	Phe	Glu	Asp	Gln	Tyr	Ser	Ile	Gly	Gly	Pro	Gln	Glu
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Gln	Ile	Thr	Val	Gln	Glu	Trp	Ser	Asp	Arg	Lys	Ser	Ala	Arg	Ser	Tyr
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140					145					150					155
Asp	Ile	Gln	Leu	Gly	Ile	Lys	Asp	Pro	Ser	Val	Phe	Thr	Pro	Pro	Ser
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			20					25					30		
Leu	Ile	Ser	Gly	Thr	Met	Lys	Val	Val	Ser	Thr	Gly	Gly	His	Asp	Leu
		35					40					45			
Ala	Ser	Gly	Glu	Phe	Ser	Tyr	Asp	Ser	Lys	Ala	Asn	Lys	Phe	Arg	Phe
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Val	Glu	Asp	Ala	Ala	His	Ala	Asn	Lys	Thr	Ser	His	Thr	Asp	Val	Leu
65					70					75					80
Val	His	Phe	Glu	Glu	Gly	Thr	Leu	Tyr	Glu	Ile	Asp	Ser	Lys	Asn	Glu
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Ser	Cys	Lys	Lys	Glu	Thr	Leu	Gln	Phe	Arg	Lys	His	Leu	Met	Glu	Ile

100					105					110					
Pro	Pro	Asp	Ala	Thr	His	Glu	Ser	Glu	Ile	Tyr	Met	Gly	Ser	Pro	Ser
		115					120					125			
Ile	Thr	Glu	Gln	Gly	Leu	Arg	Val	Arg	Val	Trp	Ser	Gly	Lys	Leu	Pro
	130					135					140				
Glu	Leu	His	Ala	His	Tyr	Ser	Leu	Ser	Ile	Thr	Ser	Cys	Gly	Cys	Leu
145					150					155					160
Pro	Val	Ser	Gly	Ser	Tyr	Tyr	Gly	Asp	Lys	Lys	Asp	Leu	Leu	Phe	Ser
				165					170					175	
Phe	Phe	Gly	Val	Glu	Thr	Glu	Val	Asp	Asp	Leu	Gln	Val	Phe	Val	Pro
			180					185					190		
Pro	Ala	Tyr	Cys	Glu	Gly	Val	Ala	Phe	Glu	Glu	Ala	Pro	Asp	Asp	His
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Ser	Phe	Phe	Asp	Leu	Phe	His	Asp								
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 <213> Oncorhynchus mykiss

<400> 4

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Asn	Met	Thr	Gly	Val	Leu	Thr	Val	Met	Ala	Leu	Thr	Gly	Gly	Glu	Ile
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Lys	Ala	Thr	Gly	His	Tyr	Ser	Tyr	Asp	Ser	Thr	Asn	Lys	Lys	Leu	Arg
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Phe	Thr	Glu	Ser	Glu	Met	His	Leu	Asn	Lys	Thr	Glu	His	Leu	Glu	Asp
65					70				75					80	
Tyr	Leu	Met	Leu	Phe	Glu	Glu	Gly	Val	Phe	Tyr	Asp	Ile	Asp	Met	Lys
				85					90					95	
Asn	Gln	Ser	Cys	Lys	Lys	Met	Ser	Leu	His	Ser	His	Ala	His	Ala	Leu
			100					105					110		
Glu	Leu	Pro	Ala	Gly	Ala	Ala	His	Gln	Val	Glu	Leu	Phe	Leu	Gly	Ser
		115					120					125			
Asp	Thr	Val	Gln	Glu	Asp	Asn	Ile	Lys	Val	Asn	Ile	Trp	Met	Gly	Ser
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Val	Ala	Glu	Thr	Lys	Gly	Gln	Tyr	Ser	Ala	Leu	Thr	Thr	Val	Gly	Glu
145					150					155					160

Cys Leu Pro Leu Ser Thr Phe Tyr Ser Thr Asp Ser Ile Thr Leu Leu
 165 170 175
 Phe Ser Asn Ser Glu Val Val Thr Glu Val Lys Ala Pro Glu Met Phe
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 195 200 205
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 210 215 220

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 <212> PRT
 <213> Cyprinus carpio

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 35 40 45
 Ser Gly Glu Phe Ser Tyr Asp Ser Lys Ala Asn Lys Phe Arg Phe Val
 50 55 60
 Glu Asp Thr Ala His Ala Asn Lys Thr Ser His Met Asp Val Leu Val
 65 70 75 80
 His Phe Glu Glu Gly Val Leu Tyr Glu Ile Asp Ser Lys Asn Glu Ser
 85 90 95
 Cys Lys Lys Glu Thr Leu Gln Phe Arg Lys His Leu Met Glu Ile Pro
 100 105 110
 Pro Asp Ala Thr His Glu Ser Glu Ile Tyr Met Gly Ser Pro Ser Ile
 115 120 125
 Thr Glu Gln Gly Leu Arg Val Arg Val Trp Asn Gly Lys Leu Pro Glu
 130 135 140
 Leu His Ala His Tyr Ser Leu Ser Thr Thr Ser Cys Gly Cys Leu Pro
 145 150 155 160
 Val Ser Gly Ser Tyr Tyr Gly Asp Lys Lys Asp Leu Leu Phe Ser Phe
 165 170 175
 Phe Gly Val Glu Thr Glu Val Asp Asp Pro Gln Val Phe Val Pro Pro
 180 185 190
 Ala Tyr Cys Glu Ala Val Ala Phe Glu Glu Ala Pro Asp Asp His Ser
 195 200 205
 Phe Phe Asp Leu Phe His Asp
 210 215

<210> 6
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 <212> PRT
 <213> Danio rerio

<400> 6
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 Ile Gly Trp Ala Ser His His Ser His Arg Gln Pro Cys His Ser Pro
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 Gln Leu Thr Ser Gly Thr Met Lys Val Val Ser Thr Gly Gly His Asp
 35 40 45
 Leu Ala Ser Gly Glu Phe Ser Tyr Asp Ser Lys Thr Asn Lys Phe Arg
 50 55 60
 Phe Val Glu Asp Thr Thr His Ala Asn Lys Thr Ser Tyr Ile Asp Val
 65 70 75 80
 Leu Ile His Phe Glu Glu Gly Val Leu Tyr Glu Ile Asp Ser Lys Asn
 85 90 95
 Glu Ser Cys Lys Lys Glu Thr Leu Gln Phe Arg Lys His Leu Met Glu
 100 105 110
 Ile Pro Val Asp Ala Thr His Glu Ser Glu Ser Tyr Met Gly Ser Pro
 115 120 125
 Ser Leu Thr Glu Gln Gly Leu Arg Val Arg Val Trp Asn Gly Lys Phe
 130 135 140
 Pro Glu Leu His Ala His Tyr Ser Leu Ser Thr Thr Ser Cys Gly Cys
 145 150 155 160
 Leu Thr Val Ser Gly Ser Tyr Tyr Gly Glu Lys Lys Asp Leu Phe Phe
 165 170 175
 Ser Phe Phe Gly Val Glu Thr Glu Val Asp Asp Leu Gln Val Phe Ala
 180 185 190
 Pro Pro Ala Tyr Cys Glu Gly Val Ser Phe Glu Glu Ala Pro Asp Asp
 195 200 205
 His Ser Phe Phe Asp Leu Phe His Asp
 210 215

<210> 7
 <211> 212
 <212> PRT
 <213> Clupea harengus

<400> 7
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Val Val Leu Ala Glu His Gln Pro Cys Arg Pro Pro Pro Gln Thr His
 20 25 30
 Gly Asn Leu Trp Val Thr Ala Ala Lys Gly Ala Pro Ala Ser Val Gly
 35 40 45
 Glu Phe Asn Tyr Asp Ser Gln Ala Arg Lys Leu His Phe Lys Asp Asp
 50 55 60
 Ala Leu His Val Asn Lys Thr Asp His Leu Glu Met Leu Ile Phe Phe
 65 70 75 80
 Glu Glu Gly Ile Phe Tyr Asp Ile Asp Ser His Asn Gln Ser Cys His
 85 90 95
 Lys Lys Thr Leu Gln Ser Thr Tyr His Cys Leu Glu Val Pro Pro Asn
 100 105 110
 Ala Thr His Val Thr Glu Gly Tyr Leu Gly Ser Glu Phe Ile Gly Asp
 115 120 125
 Gln Gly Val Arg Met Arg Lys Trp Arg Lys Arg Val Pro Glu Leu Asp
 130 135 140
 Gly Val Val Thr Val Ala Thr Thr Ser Cys Gly Cys Val Thr Leu Phe
 145 150 155 160
 Ala Thr Leu Phe Thr Asp Ser Asn Asp Val Leu Val Phe Asn Phe Leu
 165 170 175
 Asp Val Glu Met Lys Val Lys Asn Pro Leu Glu Val Phe Val Pro Pro
 180 185 190
 Ser Tyr Cys Asp Gly Val Ala Leu Glu Glu Glu Gly Asp Thr Phe Phe
 195 200 205
 Gly Leu Phe His
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<210> 8
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 <213> Artificial sequence

<220>
 <223> Contains an Nde I restriction site

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24

<210> 9
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an Asp 718 restriction site

<400> 9
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<210> 10
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an XbaI restriction site and an efficient signal
 for initiation of translation in eukaryotic cells (Kozak,
 M., J. Mol. Biol. 196:947-950 (1987))

<400> 10
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<210> 11
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an Asp 718 restriction site

<400> 11
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<210> 12
 <211> 42
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains an Asp 718 restriction site, a Kozak sequence, and
 an AUG start codon

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<210> 13
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Contains a BamHI restriction site

<400> 13
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<210> 14
 <211> 51
 <212> DNA
 <213> Artificial sequence

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<220>
<223> Contains an XbaI restriction site, a Kozak sequence, and
      an AUG start codon

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<210> 15
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<212> DNA
<213> Homo sapiens

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<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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<222> (465)..(465)
<223> n equals a, t, g or c

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<222> (490)..(490)
<223> n equals a, t, g or c

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<222> (501)..(502)
<223> n equals a, t, g or c

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gcatgcattt ctcaacaataa ttattaagct gtgtgataat ttctgctttc aggacactca 120
tccattatct tggctgtgag ctccttgggt acgggtacct tgtatgttta attttatatc 180

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cctagcacaa agcaagtgcc tggcacatag tcagtgcctt aagtatttgt agagtgaaga 240
atgccagcct ctcttgtccc tggtttcctt atgtgttgaa tgtggttgag tttgtccatt 300
gctaggggaga gacttccagt aataaaatctt actattctag atgntctact gtantgttta 360
tctgcccatt tatcttctta gtaccagggg aaagtgtgnc accctttttt aatggnaaca 420
acttnttacc taaggttacc cttttaacaa attaatgcat taagnatctt ggaatgtggc 480
ttgaaaaaan gggaactggt nnaggg                                     506

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<212> DNA
<213> Homo sapiens

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<223> n equals a, t, g or c

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<220>
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<222> (271)..(271)
<223> n equals a, t, g or c

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<220>
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<223> n equals a, t, g or c

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<220>
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<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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<220>
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<222> (339)..(339)
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<222> (348)..(348)
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<223> n equals a, t, g or c

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<222> (370)..(370)
<223> n equals a, t, g or c

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<222> (375)..(375)
<223> n equals a, t, g or c

<220>
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<222> (383)..(383)
<223> n equals a, t, g or c

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<223> n equals a, t, g or c

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taagcttctt ttttttctat gcaagagtat tgatgtatgt nctgaatctt cacagacttg 120
tcaatacaca ggcagtattc taaaatagca ctgaacaggg agtcaggaga ctattgtctc 180
ctaaacccag gactagagtt cctcgtact gtcactcctt tggtcattaa atgcactggg 240
cttgcccgca ctttggcctt cctagaacgt ngnttcaaaa cctnnttggt ctgacttttg 300
naattccctt ccagggnang tcattcanaa ggggttttnc caagcctngg tgggttnaac 360
ctgnaatttn gggangtttt ttnaaaaaat ttaaggggg ggnaaattt 409

<210> 17
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<212> DNA
<213> Homo sapiens

<220>

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aaaagcagag tgatttttgt caattttatt attaattctt aaattccctg cagagaatgc 120
ccccctttatt gctgcaccag ggtgggcatt gctcccactg agccctactc caccctgtcc 180
ctgcactccc ttggttgcca aaaaaatgat aacttaaadc ccttcagac ttaagaattt 240
tatgggcatg gnccaattga tattaaacat ttagaaggga atgaaagctt aaataggagg 300
taattattcc 310

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<210> 18
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<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
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<223> n equals a, t, g or c

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<220>
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<222> (265)..(265)
<223> n equals a, t, g or c

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<220>
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<222> (276)..(276)
<223> n equals a, t, g or c

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<220>
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<222> (287)..(287)
<223> n equals a, t, g or c

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<220>
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<222> (372)..(372)
<223> n equals a, t, g or c

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<220>
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<222> (383)..(384)
<223> n equals a, t, g or c

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<220>
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<222> (397)..(397)
<223> n equals a, t, g or c

<220>
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<222> (401)..(401)
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<223> n equals a, t, g or c

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<222> (414)..(414)
<223> n equals a, t, g or c

<220>
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<222> (417)..(417)
<223> n equals a, t, g or c

<220>
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<222> (439)..(440)
<223> n equals a, t, g or c

<220>
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<223> n equals a, t, g or c

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cccttataac caagattatc catatttatt gcaaaagcaa caatatcaaa gaatgcttta 120

aaatgcaatt gaaatttggt taatatagat aaactataag taataagatt gttttcatta 180

taatataggt gtcacacatt tctcctggta actaaggaaa gataaatggg cagataaaac 240

ataacagtag aagcatctag gattngtta ttttntttac tgggagngct cttccctagg 300

cattttacca acttcaacca ctttcaacac ataggggaac ccagggccca gggggggctg 360

ggcatttttc antttggggg ttnnttgggg cccggcnttt ntgcccgggn ttgnttntgg 420

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<210> 19
<211> 382
<212> DNA
<213> Homo sapiens

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 <223> n equals a, t, g or c

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 <222> (268)..(268)
 <223> n equals a, t, g or c

<220>
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 ttggtgtata aggatggagt gatgtttcaa attgaccaag ccaccaagca gtgctcaaag 180
 ccctgacaca gccctgggat cctcttgaca ttcctcaaaa ctccaccttt gaagaccagt 240
 actccattgg ggggcctcag gagccagntc accgtccagn agtggtcggg cagaaagtca 300
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acaatgctgt aataaataaa gtgtttcatg tgatcaaaat canntttgtt atcctctctc 180
aaaagcctgc tctccctctt accttccta aactccagtg tccatttgcc aaggccagaa 240
gcttccaagt cattcttgga tccatttgtc tccctcagtc ctcaactgggc agtncaatat 300
cccgagtcct attcaaaata gcttctttaa aactttntgc ctgtttcttc cactnccttg 360
nccctcaggc caggggccct gctgggaagg gggctggcat ntttcctgtt cagnccctggg 420
gtttnccatg ggtggactgg gngtgacgga ggccacctgg ngggtt 465